Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:55:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230407.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6230407 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230407.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:55:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230407.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,556,879
Mapped reads	3,048,909 / 85.72%
Unmapped reads	507,970 / 14.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,906 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	233,721 / 6.57%
Duplication rate	6%
Clipped reads	1,722,169 / 48.42%

2.2. ACGT Content

Number/percentage of A's	52,704,424 / 26.96%
Number/percentage of C's	35,242,586 / 18.03%
Number/percentage of T's	62,415,627 / 31.93%
Number/percentage of G's	45,026,220 / 23.03%
Number/percentage of N's	95,761 / 0.05%
GC Percentage	41.06%

2.3. Coverage

Mean	0.0632

Standard Deviation	0.5701

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

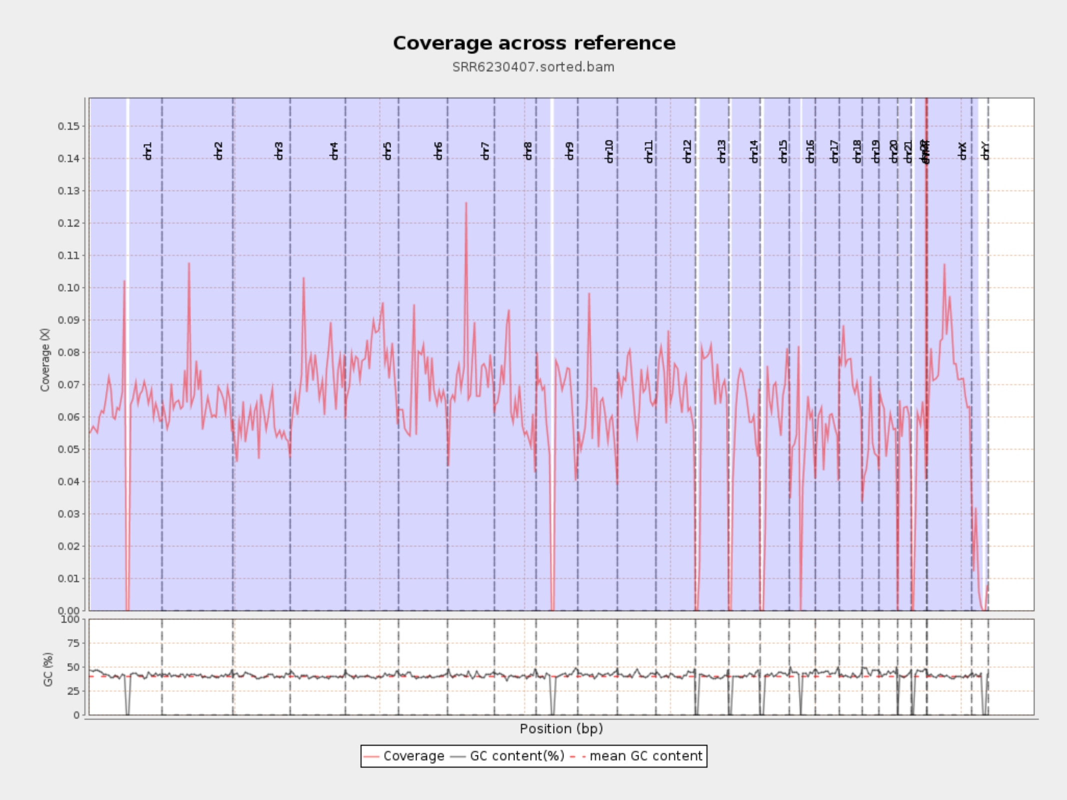
General error rate	0.89%
Mismatches	1,709,462
Insertions	16,165
Mapped reads with at least one insertion	0.53%
Deletions	49,486
Mapped reads with at least one deletion	1.61%
Homopolymer indels	46.44%

2.6. Chromosome stats

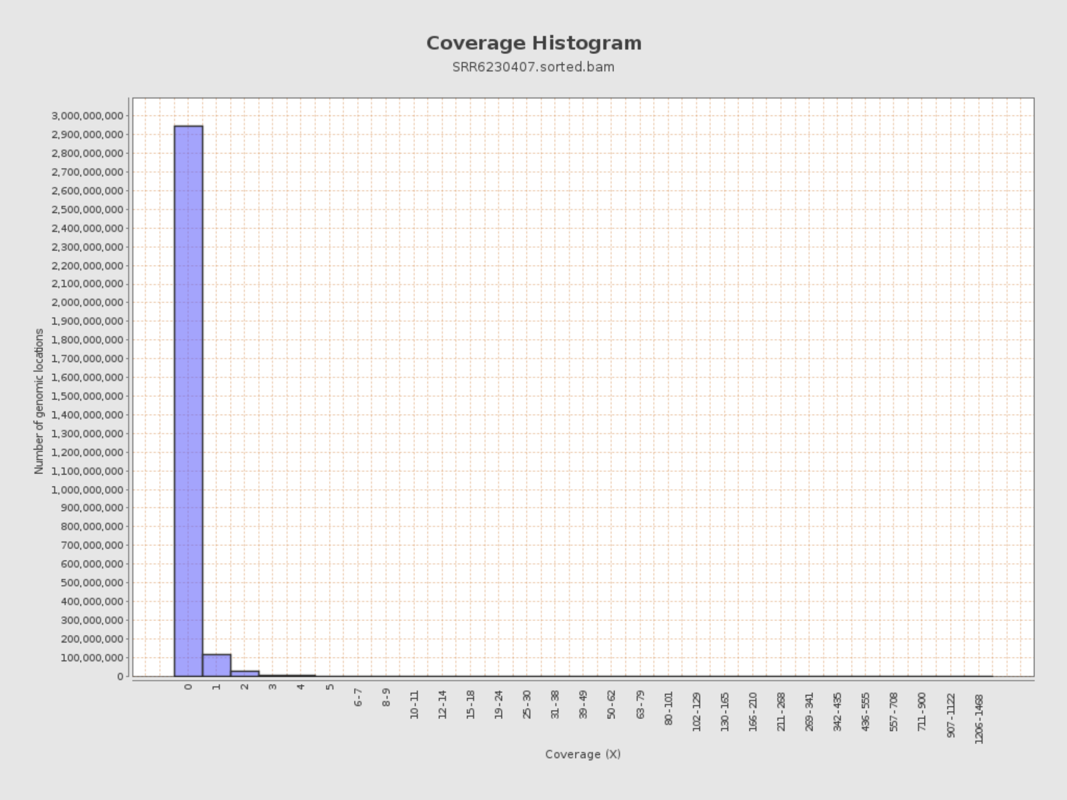
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15112490	0.0606	0.9186
chr2	243199373	16012078	0.0658	0.7227
chr3	198022430	11362627	0.0574	0.3017
chr4	191154276	13919277	0.0728	0.3951
chr5	180915260	14201693	0.0785	0.3534
chr6	171115067	11716783	0.0685	0.4189
chr7	159138663	11752298	0.0738	0.7648

chr8	146364022	9359973	0.0639	0.9578
chr9	141213431	8350842	0.0591	0.519
chr10	135534747	8186481	0.0604	0.4979
chr11	135006516	9201759	0.0682	0.5567
chr12	133851895	9205589	0.0688	0.3385
chr13	115169878	7016515	0.0609	0.3129
chr14	107349540	5771465	0.0538	0.325
chr15	102531392	5613868	0.0548	0.3041
chr16	90354753	4559296	0.0505	0.3279
chr17	81195210	4488812	0.0553	0.3477
chr18	78077248	5759677	0.0738	0.9971
chr19	59128983	2943700	0.0498	0.6418
chr20	63025520	3617244	0.0574	0.3382
chr21	48129895	2566823	0.0533	0.3277
chr22	51304566	2146110	0.0418	0.2534
chrMT	16571	377265	22.7666	18.2177
chrX	155270560	11736832	0.0756	0.4079
chrY	59373566	585450	0.0099	0.2085

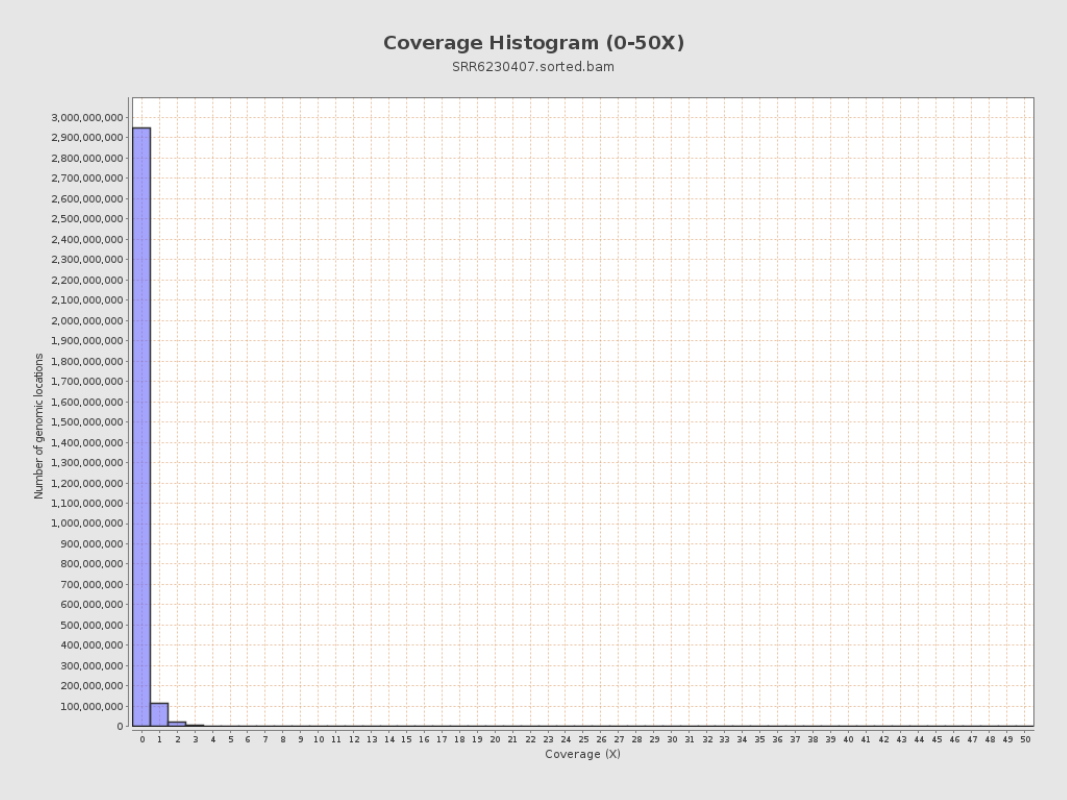
3. Results : Coverage across reference



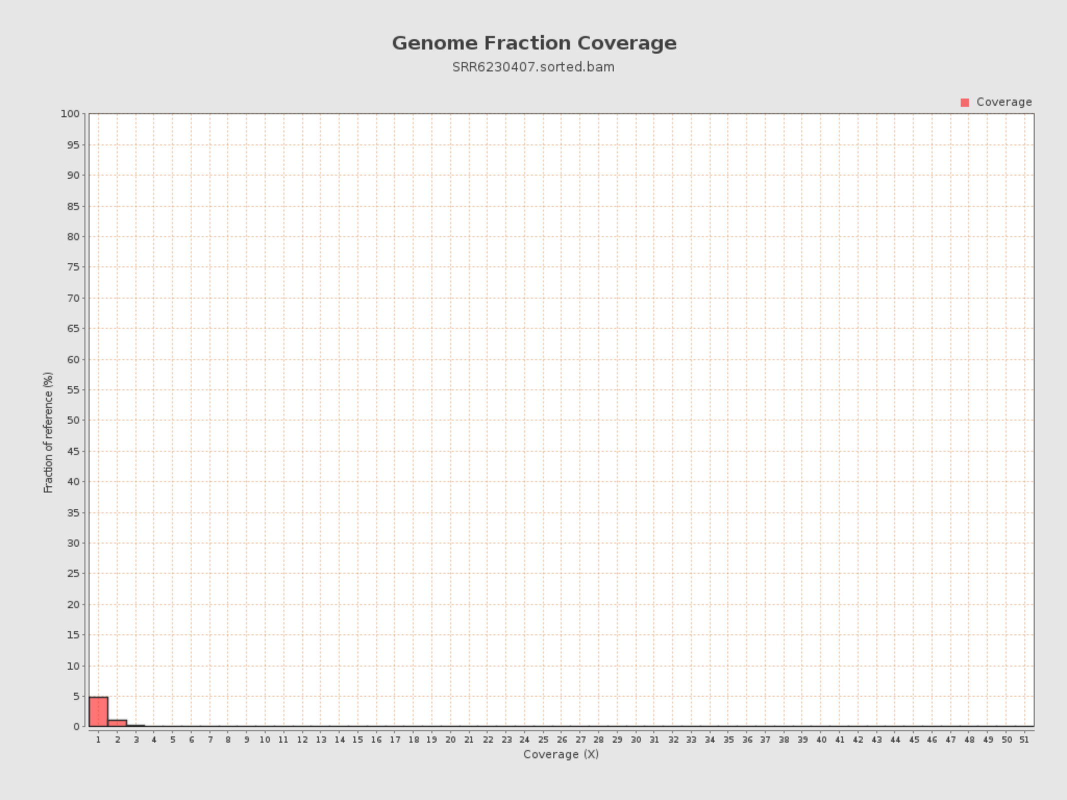
4. Results : Coverage Histogram



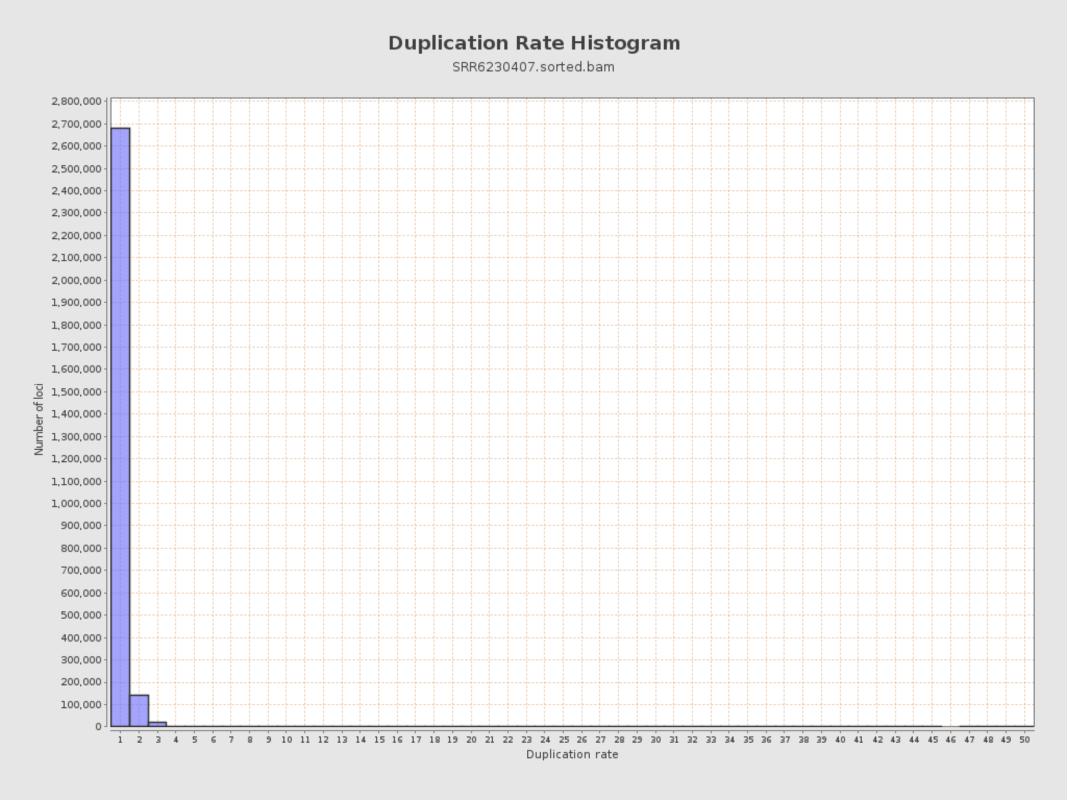
5. Results : Coverage Histogram (0-50X)



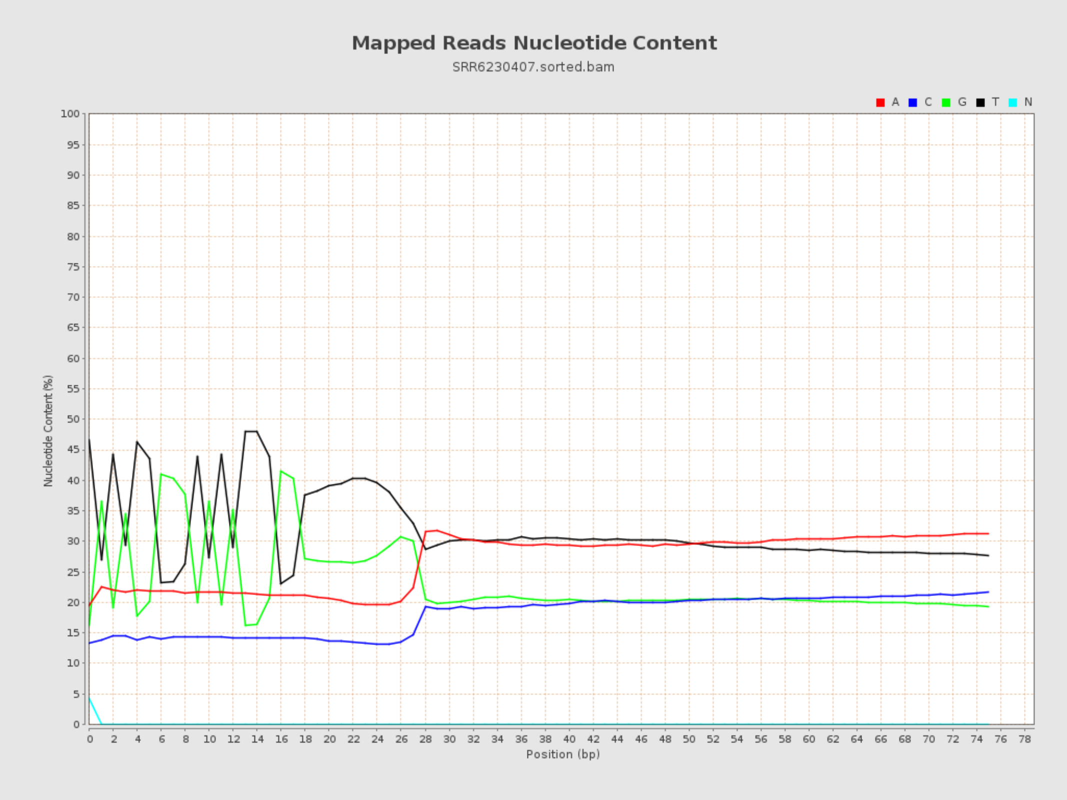
6. Results : Genome Fraction Coverage



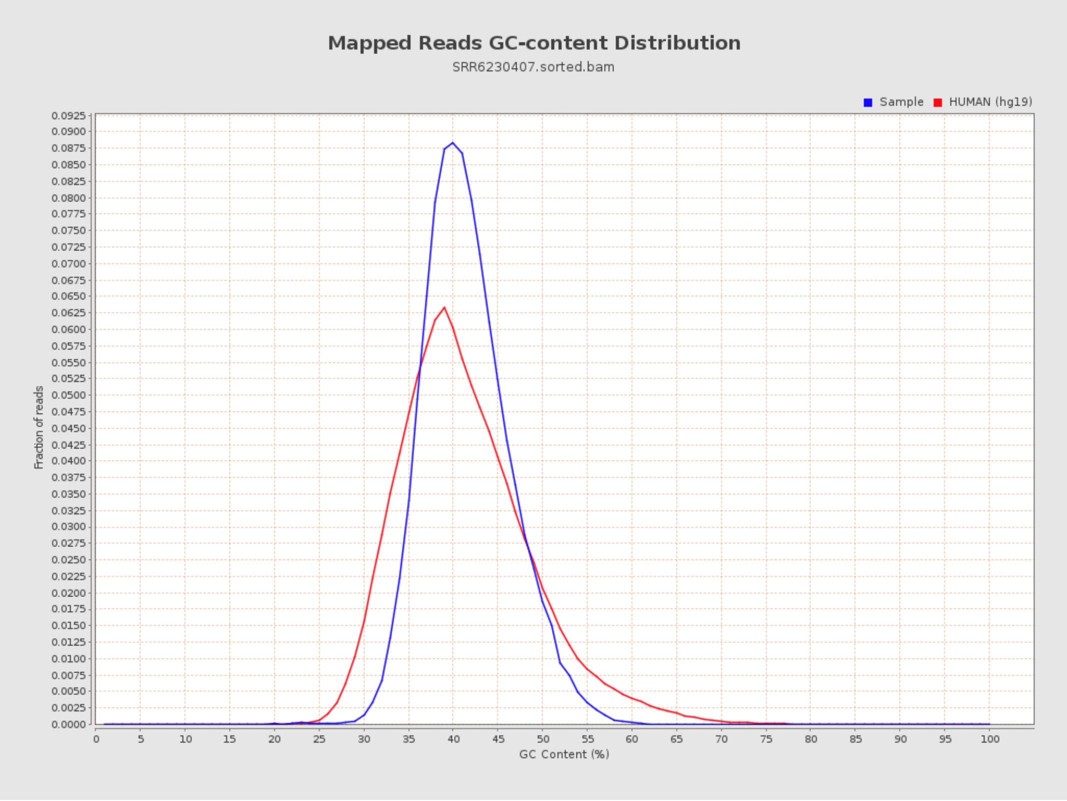
7. Results : Duplication Rate Histogram



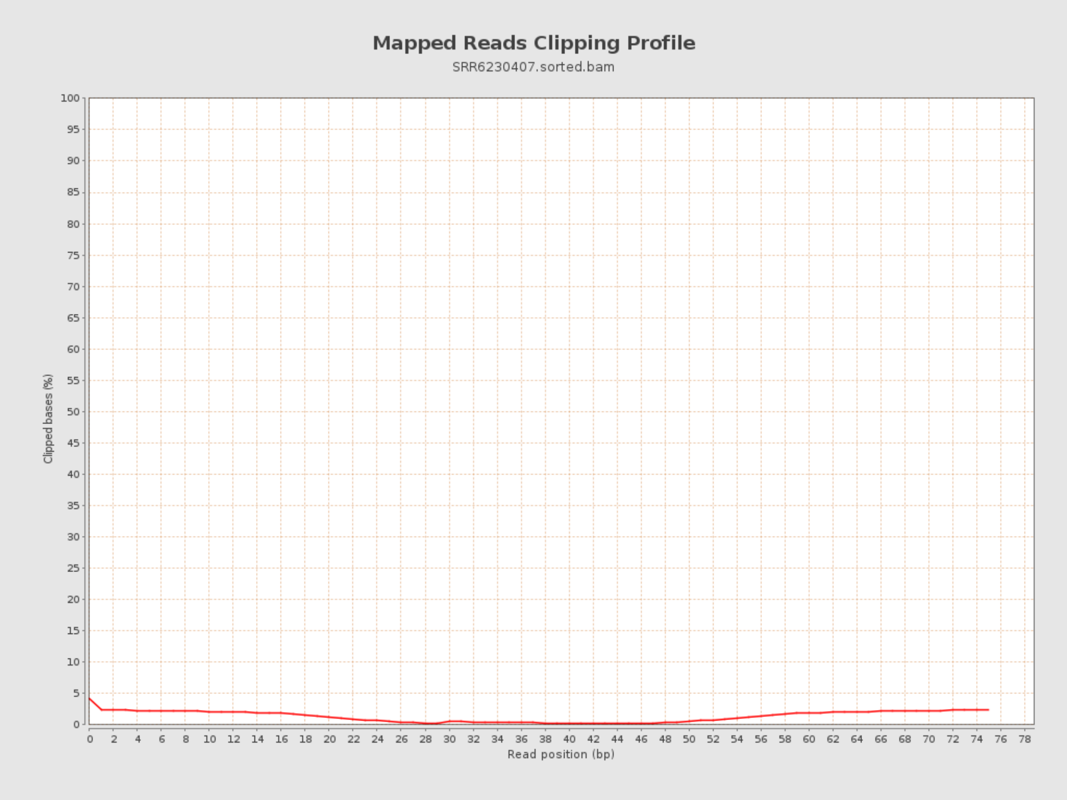
8. Results : Mapped Reads Nucleotide Content



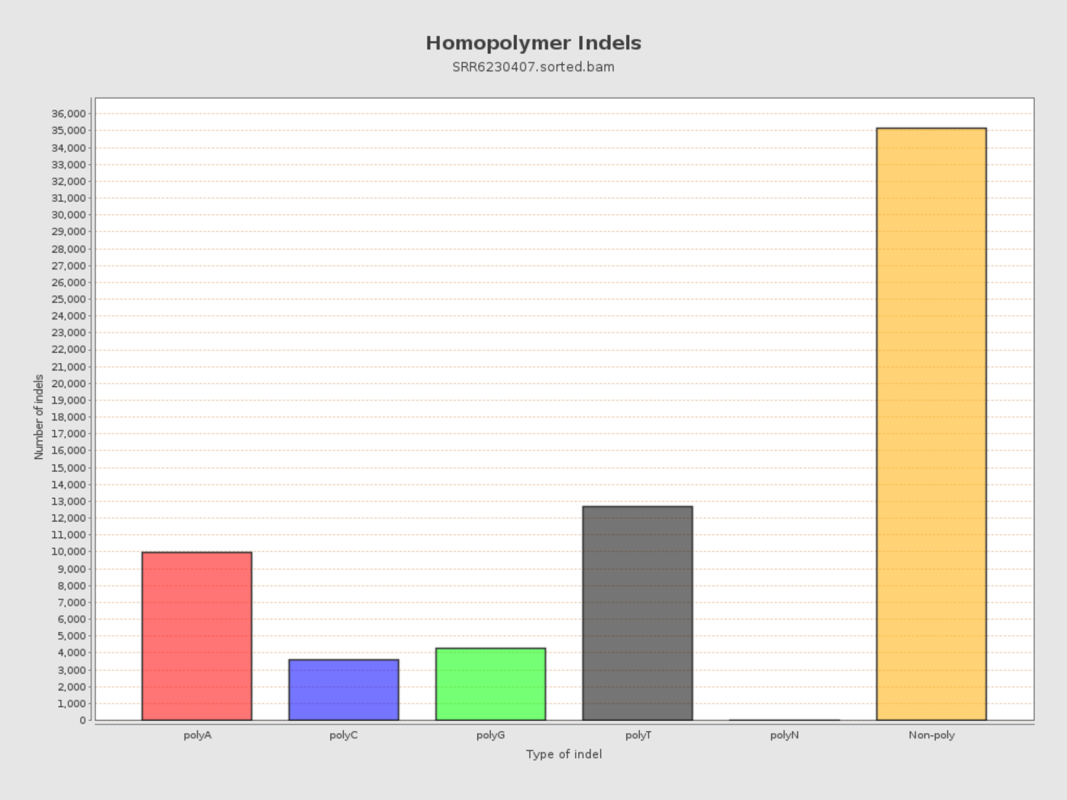
9. Results : Mapped Reads GC-content Distribution



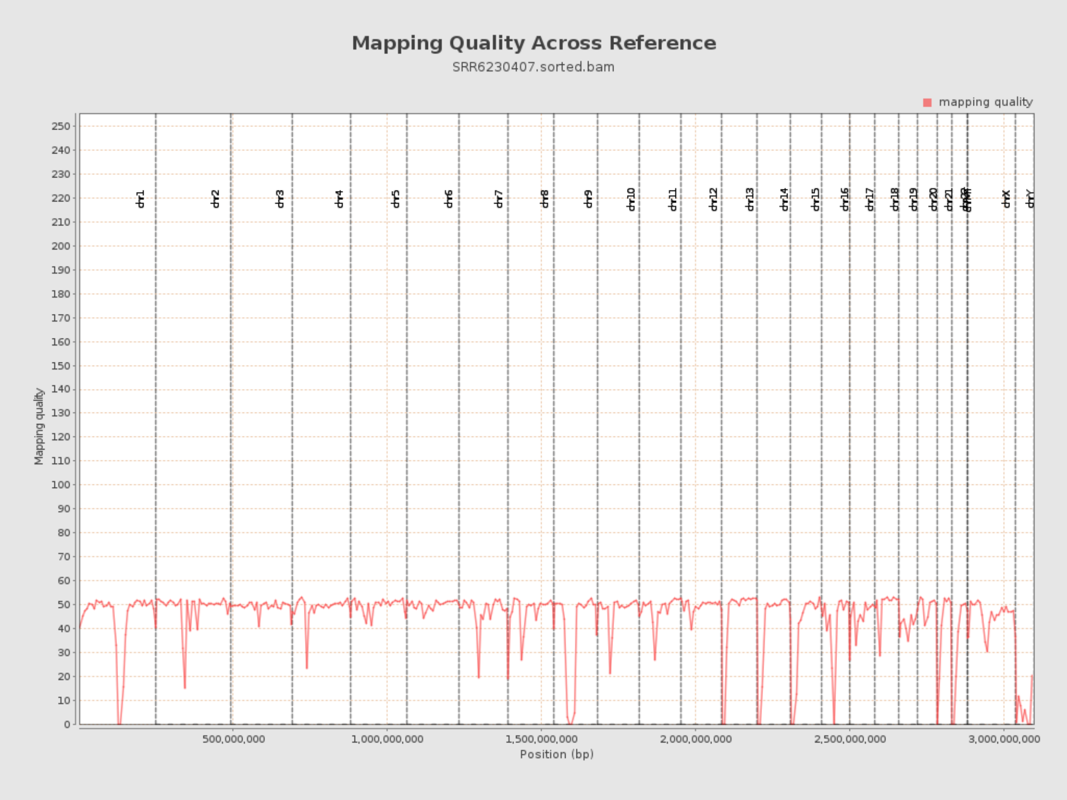
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram